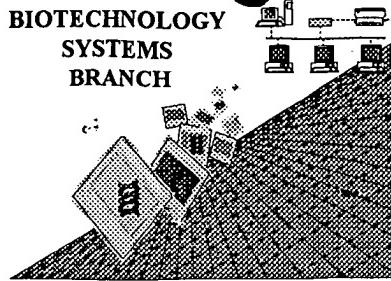


h.l.a.

RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/595,326A
Source: 1638 RUSH
Date Processed by STIC: 5/31/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/595,326A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- | | | | |
|----|---|--|-----------------------|
| 1 | ____ Wrapped Nucleic | The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping". | TECH CENTER 1600/2900 |
| 2 | ____ Wrapped Aminos | The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping". | JUN 04 2001 |
| 3 | ____ Incorrect Line Length | The rules require that a line not exceed 72 characters in length. This includes spaces. | RECEIVED |
| 4 | ____ Misaligned Amino Acid Numbering | The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers. | |
| 5 | ____ Non-ASCII | This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed. | |
| 6 | ____ Variable Length | Sequence(s) ____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing. | |
| 7 | ____ PatentIn ver. 2.0 "bug" | A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences. | |
| 8 | ____ Skipped Sequences
(OLD RULES) | Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s). | |
| 9 | ____ Skipped Sequences
(NEW RULES) | Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000 | |
| 10 | ____ Use of n's or Xaa's
(NEW RULES) | Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents. | |
| 11 | ____ Use of "Artificial"
(NEW RULES) | Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules.
Valid response is Artificial Sequence. | |
| 12 | ____ Use of <220>Feature
(NEW RULES) | Sequence(s) ____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial Sequence" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules) | |
| 13 | ____ PatentIn ver. 2.0 "bug" | Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk. | |

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/595,326A

DATE: 05/31/2001
TIME: 12:15:54

pp 1-5

Input Set : C:\PTO.txt
Output Set: C:\CRF3\05312001\I595326A.raw

Does Not Comply
Corrected Diskette Needed

3 <110> APPLICANT: ALEXANDROV, Nickolai
 4 TROUKHAN, Maxim
 6 <120> TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding
 Polypeptides Encoded
 7 Thereby
 9 <130> FILE REFERENCE: 2750-0942P
 11 <140> CURRENT APPLICATION NUMBER: 09/595,326A
 12 <141> CURRENT FILING DATE: 2000-06-16
 14 <160> NUMBER OF SEQ ID NOS: 769
 16 <170> SOFTWARE: PatentIn version 3.0
 18 <210> SEQ ID NO: 1.
 19 <211> LENGTH: 5 *invalid - per 1.823 of Sequence Rules, the only valid*
 20 <212> TYPE: PRT
 21 <213> ORGANISM: Consensus Sequence *(one of the three)*
 23 <400> SEQUENCE: 1
 25 Leu Ile Val Met Thr
 26 1 5
 28 <210> SEQ ID NO: 2
 29 <211> LENGTH: 5
 30 <212> TYPE: PRT
 31 <213> ORGANISM: Consensus Sequence *(one of the three)*
 33 <400> SEQUENCE: 2
 35 Leu Ile Val Met Phe
 36 1 5
 38 <210> SEQ ID NO: 3
 39 <211> LENGTH: 5
 40 <212> TYPE: PRT
 41 <213> ORGANISM: Consensus Sequence *(one of the three)*
 43 <400> SEQUENCE: 3
 45 Gly Ala Thr Met Cys
 46 1 5
 48 <210> SEQ ID NO: 4
 49 <211> LENGTH: 4
 50 <212> TYPE: PRT
 51 <213> ORGANISM: Consensus Sequence *(one of the three)*
 53 <400> SEQUENCE: 4
 55 Leu Ile Val Met
 56 1
 58 <210> SEQ ID NO: 5
 59 <211> LENGTH: 4
 60 <212> TYPE: PRT
 61 <213> ORGANISM: Consensus Sequence *(one of the three)*
 63 <400> SEQUENCE: 5
 65 Leu Ile Phe Ala
 66 1
 68 <210> SEQ ID NO: 6
 69 <211> LENGTH: 7
 70 <212> TYPE: PRT

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/595,326A

DATE: 05/31/2001
TIME: 12:15:54

Input Set : C:\PTO.txt
Output Set: C:\CRF3\05312001\I595326A.raw

71 <213> ORGANISM: Consensus Sequence
73 <400> SEQUENCE: 6
75 Leu Ile Val Met Phe Tyr Cys
76 1 5
78 <210> SEQ ID NO: 7
79 <211> LENGTH: 11
80 <212> TYPE: PRT
81 <213> ORGANISM: Consensus Sequence
83 <400> SEQUENCE: 7
85 Ser Ala Pro Gly Leu Val Phe Tyr Lys Gln His
86 1 5 10
88 <210> SEQ ID NO: 8
89 <211> LENGTH: 6
90 <212> TYPE: PRT
91 <213> ORGANISM: Consensus Sequence
93 <400> SEQUENCE: 8
95 Asp Glu Asn Gln Met Trp
96 1 5
98 <210> SEQ ID NO: 9
99 <211> LENGTH: 12
100 <212> TYPE: PRT
101 <213> ORGANISM: Consensus Sequence
103 <400> SEQUENCE: 9
105 Lys Arg Gln Ala Ser Pro Cys Leu Ile Met Phe Trp
106 1 5 10
108 <210> SEQ ID NO: 10
109 <211> LENGTH: 9
110 <212> TYPE: PRT
111 <213> ORGANISM: Consensus Sequence
113 <400> SEQUENCE: 10
115 Lys Arg Asn Gln Ser Thr Ala Val Met
116 1 5
118 <210> SEQ ID NO: 11
119 <211> LENGTH: 7
120 <212> TYPE: PRT
121 <213> ORGANISM: Consensus Sequence
123 <400> SEQUENCE: 11
125 Lys Arg Ala Cys Leu Val Met
126 1 5
128 <210> SEQ ID NO: 12
129 <211> LENGTH: 9
130 <212> TYPE: PRT
131 <213> ORGANISM: Consensus Sequence
133 <400> SEQUENCE: 12
135 Leu Ile Val Met Phe Tyr Pro Ala Asn
136 1 5
138 <210> SEQ ID NO: 13
139 <211> LENGTH: 6
140 <212> TYPE: PRT

RAW SEQUENCE LISTING
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TIME: 12:15:54

Input Set : C:\PTO.txt
Output Set: C:\CRF3\05312001\I595326A.raw

141 <213> ORGANISM: Consensus Sequence
143 <400> SEQUENCE: 13
145 Leu Ile Val Met Phe Trp
146 1 5
148 <210> SEQ ID NO: 14
149 <211> LENGTH: 8
150 <212> TYPE: PRT
151 <213> ORGANISM: Consensus Sequence
153 <400> SEQUENCE: 14
155 Ser Ala Gly Cys Leu Ile Val Pro
156 1 5
158 <210> SEQ ID NO: 15
159 <211> LENGTH: 5
160 <212> TYPE: PRT
161 <213> ORGANISM: Consensus Sequence
163 <400> SEQUENCE: 15
165 Phe Tyr Trp His Pro
166 1 5
168 <210> SEQ ID NO: 16
169 <211> LENGTH: 4
170 <212> TYPE: PRT
171 <213> ORGANISM: Consensus Sequence
173 <400> SEQUENCE: 16
175 Lys Arg His Pro
176 1
178 <210> SEQ ID NO: 17
179 <211> LENGTH: 10
180 <212> TYPE: PRT
181 <213> ORGANISM: Consensus Sequence
183 <400> SEQUENCE: 17
185 Leu Ile Val Met Phe Tyr Trp Ser Thr Ala
186 1 5 10
188 <210> SEQ ID NO: 18
189 <211> LENGTH: 6
190 <212> TYPE: PRT
191 <213> ORGANISM: Consensus Sequence
193 <400> SEQUENCE: 18
195 Leu Ile Val Met Phe Tyr
196 1 5
198 <210> SEQ ID NO: 19
199 <211> LENGTH: 4
200 <212> TYPE: PRT
201 <213> ORGANISM: Consensus Sequence
203 <400> SEQUENCE: 19
205 Gly Ser Thr Ala
206 1
208 <210> SEQ ID NO: 20
209 <211> LENGTH: 4
210 <212> TYPE: PRT

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/595,326A

DATE: 05/31/2001
TIME: 12:15:54

Input Set : C:\PTO.txt
Output Set: C:\CRF3\05312001\I595326A.raw

211 <213> ORGANISM: Consensus Sequence
213 <400> SEQUENCE: 20

215 Ser Thr Ala Gly
216 1

218 <210> SEQ ID NO: 21

219 <211> LENGTH: 4

220 <212> TYPE: PRT

221 <213> ORGANISM: Consensus Sequence
223 <400> SEQUENCE: 21

225 Ser Thr Glu Ile

226 1

228 <210> SEQ ID NO: 22

229 <211> LENGTH: 7

230 <212> TYPE: PRT

231 <213> ORGANISM: Consensus Sequence
233 <400> SEQUENCE: 22

235 Pro Ala Ser Leu Ile Val Met

236 1 5

238 <210> SEQ ID NO: 23

239 <211> LENGTH: 4

240 <212> TYPE: PRT

241 <213> ORGANISM: Consensus Sequence
243 <400> SEQUENCE: 23

245 Ser Ala Lys Arg

246 1

248 <210> SEQ ID NO: 24

249 <211> LENGTH: 5

250 <212> TYPE: PRT

251 <213> ORGANISM: Consensus Sequence
253 <400> SEQUENCE: 24

255 Ser Thr Ala Gly Asn

256 1 5

258 <210> SEQ ID NO: 25

259 <211> LENGTH: 4

260 <212> TYPE: PRT

261 <213> ORGANISM: Consensus Sequence
263 <400> SEQUENCE: 25

265 Ser Ala Gly Val

266 1

268 <210> SEQ ID NO: 26

269 <211> LENGTH: 7

270 <212> TYPE: PRT

271 <213> ORGANISM: Consensus Sequence
273 <400> SEQUENCE: 26

275 Leu Ile Val Met Phe Tyr Trp

276 1 5

278 <210> SEQ ID NO: 27

279 <211> LENGTH: 7

280 <212> TYPE: PRT

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/595,326A

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TIME: 12:15:54

Input Set : C:\PTO.txt
Output Set: C:\CRF3\05312001\I595326A.raw

281 <213> ORGANISM: Consensus Sequence
283 <400> SEQUENCE: 27
285 Gly Ser Ala Cys Ile Val Met
286 1 5
288 <210> SEQ ID NO: 28
289 <211> LENGTH: 4
290 <212> TYPE: PRT
291 <213> ORGANISM: Consensus Sequence
293 <400> SEQUENCE: 28
295 Gly Thr Ile Val
296 1
298 <210> SEQ ID NO: 29
299 <211> LENGTH: 6
300 <212> TYPE: PRT
301 <213> ORGANISM: Consensus Sequence
303 <400> SEQUENCE: 29
305 Gly Ser Thr Ala Asn Ile
306 1 5
308 <210> SEQ ID NO: 30
309 <211> LENGTH: 5
310 <212> TYPE: PRT
311 <213> ORGANISM: Consensus Sequence
313 <400> SEQUENCE: 30
315 Leu Ile Val Met Ala
316 1 5
318 <210> SEQ ID NO: 31
319 <211> LENGTH: 6
320 <212> TYPE: PRT
321 <213> ORGANISM: Consensus Sequence
323 <400> SEQUENCE: 31
325 Leu Ile Val Trp Pro Gln
326 1 5
328 <210> SEQ ID NO: 32
329 <211> LENGTH: 5
330 <212> TYPE: PRT
331 <213> ORGANISM: Consensus Sequence
333 <400> SEQUENCE: 32
335 Gly Ser Thr Ala Met
336 1 5
338 <210> SEQ ID NO: 33
339 <211> LENGTH: 6
340 <212> TYPE: PRT
341 <213> ORGANISM: Consensus Sequence
343 <400> SEQUENCE: 33
345 Leu Ile Met Pro Thr Ala
346 1 5
348 <210> SEQ ID NO: 34
349 <211> LENGTH: 4
350 <212> TYPE: PRT

Please correct this error
in subsequent sequences.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/595,326A

DATE: 05/31/2001

TIME: 12:15:55

Input Set : C:\PTO.txt

Output Set: C:\CRF3\05312001\I595326A.raw